

Dev

1641

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/905,293

DATE: 01/28/99
TIME: 12:12:21

INPUT SET: S30969.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information
4
5 (i) APPLICANT: Yelton, Dale E.
6 Rosok, Mae Joanne
7
8 (ii) TITLE OF THE INVENTION: A METHOD FOR INHIBITING IMMUNOGLOBULIN-
9
10 (iii) NUMBER OF SEQUENCES: 27
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
14 (B) STREET: 11150 Santa Monica Boulevard, Suite 400
15 (C) CITY: Los Angeles
16 (D) STATE: CA
17 (E) COUNTRY: USA
18 (F) ZIP: 90025
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Diskette
22 (B) COMPUTER: IBM Compatible
23 (C) OPERATING SYSTEM: DOS
24 (D) SOFTWARE: FastSEQ for Windows Version 2.0
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 08/905,293
28 (B) FILING DATE: 01-AUG-1997
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: 60/023,033
33 (B) FILING DATE: 02-AUG-1996
34
35
36
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Canady, Karen S
39 (B) REGISTRATION NUMBER: 39,927
40 (C) REFERENCE/DOCKET NUMBER: 30436.43USU1
41
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 310-445-1140
44 (B) TELEFAX: 310-445-9031
45 (C) TELEX:
46

RAW SEQUENCE LISTING
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47
48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 36 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: cDNA
57
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60 TGGCACCAGAA AGCTTTCTGG GGCAGGCCAG GCCTGA 36
61
62 (2) INFORMATION FOR SEQ ID NO:2:
63
64 (i) SEQUENCE CHARACTERISTICS:
65 (A) LENGTH: 57 base pairs
66 (B) TYPE: nucleic acid
67 (C) STRANDEDNESS: single
68 (D) TOPOLOGY: linear
69
70 (ii) MOLECULE TYPE: cDNA
71
72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
73
74 TCCGGACATG TTGGTACCCA CGTGGTGGTC GACGCTGAGC CTGGCTTCGA GCAGACA 57
75
76 (2) INFORMATION FOR SEQ ID NO:3:
77
78 (i) SEQUENCE CHARACTERISTICS:
79 (A) LENGTH: 55 base pairs
80 (B) TYPE: nucleic acid
81 (C) STRANDEDNESS: single
82 (D) TOPOLOGY: linear
83
84 (ii) MOLECULE TYPE: cDNA
85
86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
87
88 GTCGACCACC ACGTGGGTAC CAACATGTCC GGAGCCACAT GGACAGAGGC CGGCT 55
89
90 (2) INFORMATION FOR SEQ ID NO:4:
91
92 (i) SEQUENCE CHARACTERISTICS:
93 (A) LENGTH: 30 base pairs
94 (B) TYPE: nucleic acid
95 (C) STRANDEDNESS: single
96 (D) TOPOLOGY: linear
97
98 (ii) MOLECULE TYPE: cDNA
99

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100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
101
102 CTGGTTCTTG GTCATCTCCT CTCTAGATGG 30
103
104 (2) INFORMATION FOR SEQ ID NO:5:
105
106 (i) SEQUENCE CHARACTERISTICS:
107 (A) LENGTH: 36 base pairs
108 (B) TYPE: nucleic acid
109 (C) STRANDEDNESS: single
110 (D) TOPOLOGY: linear
111
112 (ii) MOLECULE TYPE: cDNA
113
114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
115
116 ACCATGGTCG ACCTCAGACC TGCCAAGAGC CATATC 36
117
118 (2) INFORMATION FOR SEQ ID NO:6:
119
120 (i) SEQUENCE CHARACTERISTICS:
121 (A) LENGTH: 40 base pairs
122 (B) TYPE: nucleic acid
123 (C) STRANDEDNESS: single
124 (D) TOPOLOGY: linear
125
126 (ii) MOLECULE TYPE: cDNA
127
128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
129
130 CATGGTCACG TGGTGTGTCC CTGGATGCAG GCTACTCTAG 40
131
132 (2) INFORMATION FOR SEQ ID NO:7:
133
134 (i) SEQUENCE CHARACTERISTICS:
135 (A) LENGTH: 49 base pairs
136 (B) TYPE: nucleic acid
137 (C) STRANDEDNESS: single
138 (D) TOPOLOGY: linear
139
140 (ii) MOLECULE TYPE: cDNA
141
142 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
143
144 CAGGGAGGGA GGGTGTCTGC TGGAAGCCAG GCTCAGCGCT GACCTCAGA 49
145
146 (2) INFORMATION FOR SEQ ID NO:8:
147
148 (i) SEQUENCE CHARACTERISTICS:
149 (A) LENGTH: 50 base pairs
150 (B) TYPE: nucleic acid
151 (C) STRANDEDNESS: single
152 (D) TOPOLOGY: linear

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153
154 (ii) MOLECULE TYPE: cDNA
155
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
157
158 GGAAAGAACC ATCACAGTCT CGCAGGGGCC CAGGGCAGCG CTGGGTGCTT 50
159
160 (2) INFORMATION FOR SEQ ID NO:9:
161
162 (i) SEQUENCE CHARACTERISTICS:
163 (A) LENGTH: 8691 base pairs
164 (B) TYPE: nucleic acid
165 (C) STRANDEDNESS: single
166 (D) TOPOLOGY: linear
167
168 (ii) MOLECULE TYPE: cDNA
169
170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
171
172 GACGGATCGG GAGATCTGCT AGGTGACCTG AGGCGCGCCG GCTTCGAATA GCCAGAGTAA 60
173 CCTTTTCTTT TAATTTTATT TTATTTTATT TTTGAGATGG AGTTTGGCGC CGATCTCCCG 120
174 ATCCCTATG GTCGACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAGTATC 180
175 TGCTCCCTGC TTGTGTGTTG GAGGTCGCTG AGTAGTGCGC GAGCAAAATT TAAGCTACAA 240
176 CAAGGCAAGG CTTGACCGAC AATTGCATGA AGAATCTGCT TAGGGTTAGG CGTTTTGCGC 300
177 TGCTTCGCGA TGTACGGGCC AGATATACGC GTTGACATTG ATTATTGACT AGTTATTAAT 360
178 AGTAATCAAT TACGGGGTCA TTAGTTTATA GCCCATATAT GGAGTTCCGC GTTACATAAC 420
179 TTACGGTAAA TGGCCCCGCT GGTGACCGC CCAACGACCC CCGCCCATTTG ACGTCAATAA 480
180 TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA TGGGTGGACT 540
181 ATTTACGGTA AACTGCCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA AGTACGCCCC 600
182 CTATTGACGT CAATGACGGT AAATGGCCCC CCTGGCATTA TGCCCAGTAC ATGACCTTAT 660
183 GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC 720
184 GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC 780
185 TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG GACTTTCCAA 840
186 AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA CGGTGGGAGG 900
187 TCTATATAAG CAGAGCTCTC TGGCTAACTA GAGAACCCAC TGCTTACTGG CTTATCGAAA 960
188 TTAATACGAC TCACTATAGG GAGACCCAAG CTTGGTACCA ATTTAAATTG ATATCTCCTT 1020
189 AGGTCTCGAG TCTCTAGATA ACCGGTCAAT CGATTGGAAT TCTTGCGGCC GCTTGCTAGC 1080
190 CACCATGGAG TTGTGGTTAA GCTTGGTCCCT TCCTTGTCCT TGTTTTAAAA GGTGTCCAGT 1140
191 GTGAAGTGAA TCTGGTGGAG TCTGGGGGAG GCTTAGTGCA GCCTGGAGGG TCCCTGAAAG 1200
192 TCTCCTGTGT AACCTCTGGA TTCACTTTCA GTGACTATTA CATGTATTGG GTTCGCCAGA 1260
193 CTCCAGAGAA GAGGCTGGAG TGGGTGCGAT ACATTAGTCA AGGTGGTGAT ATAACCGACT 1320
194 ATCCAGACAC TGTAAGGGGT CGATTACCA TCTCCAGAGA CAATGCCAAG AACACCCCTGT 1380
195 ACCTGCAAAT GAGCCGTCTG AAGTCTGAGG ACACAGCCAT GTATTACTGT GCAAGAGGCC 1440
196 TGGACGACGG GGCTTGGTTT GCTTACTGGG GCCAAGGGAC TCTGGTCACG GTCTCTGTAG 1500
197 CTAGCACCAA GGGCCCATCG GTCTTCCCCC TGGCACCCCT CTCCAAGAGC ACCTCTGGGG 1560
198 GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCAGGTG ACGGTGTCTG 1620
199 GGAATCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCTTA CAGTCCCTCAG 1680
200 GACTCTACTC CCTCAGCAGC GTGGTCAACG TGCCCTCCAG CAGCTTGGGC ACCCAGACCT 1740
201 ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT GGACAAGAAA GTTGGTGAGA 1800
202 GGCCAGACA GGGAGGAGG GTGTCTGCTG GAAGCCAGG TCACCGCTCC TGCTTGGACG 1860
203 CATCCCGGCT ATGCAGCCCC AGTCTAGGGC AGCAAGGCAG GCGCCGCTCTG CCTCTTCAAC 1920
204 CGGAGGCCTC TGCCCGCCCC ACTCATGCTC AGGGAGAGGG TCTTCTGGCT TTTTCCCCAG 1980
205 GCTCTGGGCA GGCACAGGCT AGGTGCCCTT AACCCAGGCC CTGCACACAA AGGGGCAGGT 2040

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206	GCTGGGCTCA	GACCTGCCAA	GAGCCATATC	CGGGAGGACC	CTGCCCCCTGA	CCTAAGCCCCA	2100
207	CCCCAAAGGC	CAAACCTCTCC	ACTCCCTCAG	CTCGGACACC	TTCTCTCTCTC	CCAGATTCCA	2160
208	GTAACCTCCCA	ATCTTCTCTC	TGCAGAGCCC	AAATCTTGTTG	ACAAAACCTCA	CACATGCCCA	2220
209	CCGTGCCCAG	GTAAGCCAGC	CCAGGCCCTCG	CCCTCCAGCT	CAAGGCGGGA	CAGGTGCCCT	2280
210	AGAGTAGCCT	GCATCCAGGG	ACAGGCCCCA	GCCGGGTGCT	GACACGTCCA	CCTCCATCTC	2340
211	TTCTCTAGCA	CCTGAACCTCC	TGGGGGGACC	GTCAGTCTTC	CTCTTCCCCC	CAAAACCCAA	2400
212	GGACACCCCTC	ATGATCTCCC	GGACCCCTGA	GGTCACATGC	GTGGTGGTGG	ACGTGAGCCA	2460
213	CGAAGACCCCT	GAGGTCAAGT	TCAACTGGTA	CGTGGACGGC	GTGGAGGTGC	ATAATGCCAA	2520
214	GACAAAGCCG	CGGGAGGAGC	AGTACAACAG	CACGTACCGT	GTGGTCAGCG	TCCTCACCCT	2580
215	CCTGCACCAG	GACTGGCTGA	ATGGCAAGGA	GTACAAGTGC	AAGGTCTCCA	ACAAAGCCCT	2640
216	CCCAGCCCCC	ATCGAGAAAA	CCATCTCCAA	AGCCAAAGGT	GGGACCCGTG	GGGTGCGGAG	2700
217	GCCACATGGA	CAGAGGCCGG	CTCGGCCAC	CCCTCTGCCCT	GAGAGTGACC	GCTGTACCAA	2760
218	CTCTGTCTCC	TACAGGGCAG	CCCCGAGAAC	CACAGGTGTA	CACCCTGCCC	CCATCCCGGG	2820
219	ATGAGCTGAC	CAAGAACCAG	GTCAGCCTGA	CTGGCTGGT	CAAAGGCTTC	TATCCAGCG	2880
220	ACATCGCCGT	GGAGTGGGAG	AGCAATGGGC	AGCCGGAGAA	CAACTACAAG	ACCACGCCCTC	2940
221	CCGTGCTGGA	CTCCGACGGC	TCCTTCTTCC	TCTACAGCAA	GCTCACCCTG	GACAAGAGCA	3000
222	GGTGGCAGCA	GGGGAACGTC	TTCTCATGCT	CCGTGATGCA	TGAGGCTCTG	CACAACCACT	3060
223	ACACGCAGAA	GAGCCTCTCC	CTGTCTCCGG	GTAAATGAGT	GCGACGGCCG	GCAAGCCCCC	3120
224	GCTCCCCGGG	CTCTCGCGGT	CGCACGAGGA	TGCTTGGCAC	GTACCCCTTG	TACATACTTC	3180
225	CCGGGCGCCC	AGCATGGAAA	TAAAGCACCC	AGCGCTGCCC	TGGGCCCTTG	CGAGACTGTG	3240
226	ATGGTTCTTT	CCACGGGTCA	GGCCGAGTCT	GAGGCCCTGAG	TGGCATGAGG	GAGGCAGAGC	3300
227	GGGTCCCACT	GTCCCCACAC	TGGCCCAGGC	TGTGCAGGTG	TGCCCTGGGCC	CCCTAGGGTG	3360
228	GGGCTCAGCC	AGGGGCTGCC	CTCGGCAGGG	TGGGGGATTT	GCCAGCGTGG	CCCTCCCTCC	3420
229	AGCAGCACCT	GCCCTGGGCT	GGGCCACGGG	AAGCCCTAGG	AGCCCTTGGG	GACAGACACA	3480
230	CAGCCCCCTGC	CTCTGTAGGA	GACTGTCTCTG	TTCTGTGAGC	GCCCCCTGTCC	TCCCGACCTC	3540
231	CATGCCCACCT	CGGGGGCATG	CCTAGTCCAT	GTGCGTAGGG	ACAGGCCCTC	CCTCACCCAT	3600
232	CTACCCCCAC	GGCACTAACC	CCTGGCTGCC	CTGCCCAGCC	TCGCACCCGC	ATGGGGACAC	3660
233	AACCGACTCC	GGGGACATGC	ACTCTCGGGC	CTGTGGAGG	GACTGGTGCA	GATGCCACACA	3720
234	CACACACTCA	GCCCAGACCC	GTTCAACAAA	CCCCGCACTG	AGGTTGGCCG	GCCACACGGC	3780
235	CACCACACAC	ACACGTGCAC	GCTTCACACA	CGGAGCCTCA	CCCGGGCGAA	CTCCACAGCA	3840
236	CCCAGACCAG	AGCAAGGTCC	TGCGACACGT	GAACACTCCT	CGGACACAGG	CCCCACGAG	3900
237	CCCCACGCGG	CACCTCAAGG	CCCACGAGCC	TCTCGGCAGC	TTCTCCACAT	GCTGACCTGC	3960
238	TCAGACAAAC	CCAGCCCTCC	TCTCACAAGG	GTGCCCCCTGC	AGCCGCCACA	CACACACAGG	4020
239	GGATCACACA	CCACGTCACG	TCCCTGGCCC	TGGCCCACTT	CCCAGTGCCG	CCCTTCCCTG	4080
240	CAGGACGGAT	CAGCCTCGAC	TGTGCCCTTCT	AGTTGCCAGC	CATCTGTTGT	TTGCCCTTCC	4140
241	CCCGTGCCCTT	CCTTGACCCCT	GGAAGGTGCC	ACTCCCACTG	TCCTTTCTTA	ATAAAATGAG	4200
242	GAAATTGCAT	CGCATTGTCT	GAGTAGGTGT	CATTCTATTCT	TGGGGGGTGG	GGTGGGGCAG	4260
243	GACAGCAAGG	GGGAGGATTG	GGAAGACAAT	AGCAGGCATG	CTGGGGATGC	GGTGGGCTCT	4320
244	ATGGCTTCTG	AGGCGGAAAG	AACCAGCTGG	GGCTCTAGGG	GGTATCCCCA	CGCGCCCTGT	4380
245	AGCGGCGCAT	TAAGCGCGGC	GGGTGTGGTG	GTTACGCGCA	GCGTGACCGC	TACACTTGCC	4440
246	AGCGCCCTAG	CGCCCGCTCC	TTTCGCTTTC	TTCCCTTCCCT	TTCTCGCCAC	GTTGCGCCGG	4500
247	CTCTCAAAA	AAGGGAAAAA	AAGCATGCAT	CTCAATTAGT	CAGCAACCAT	AGTCCCGCCC	4560
248	CTAACTCCGC	CCATCCCGCC	CCTAACTCCG	CCAGTTCCG	CCCATCTCTC	GCCCCATGGC	4620
249	TGACTAATTT	TTTTTTATTTA	TGCAGAGGCC	GAGGCCGCCCT	CGGCCCTCTGA	GCTATTCCAG	4680
250	AAGTAGTGAG	GAGGCTTTTTT	TGGAGGCCCTA	GGCTTTTGTGA	AAAAGCTTGG	ACAGCTCAGG	4740
251	GCTGCGATTT	CGCGCCAAAC	TTGACGGCAA	TCCTAGCGTG	AAGGCTGGTA	GGATTTTATC	4800
252	CCCGCTGCCA	TCATGGTTCTG	ACCATTTGAAC	TGCATCGTCG	CCGTGTCCCA	AAATATGGGG	4860
253	ATTGGCAAGA	ACGGAGACCT	ACCCCTGGCCT	CCGCTCAGGA	ACGAGTTCAA	GTACTTCCAA	4920
254	AGAATGACCA	CAACCTCTTC	AGTGGAAGGT	AAACAGAATC	TGGTGATTAT	GGGTAGGAAA	4980
255	ACCTGGTTCT	CCATTCCCTGA	GAAGAATCGA	CCTTTAAAGG	ACAGAATTAA	TATAGTTCTC	5040
256	AGTAGAGAAC	TCAAAGAACC	ACCACGAGGA	GCTCATTTTTT	TTGCCAAAAG	TTTGGATGAT	5100
257	GCCTTAAGAC	TTATTGAACA	ACCGGAATTG	GCAAGTAAAG	TAGACATGGT	TTGGATAGTC	5160
258	GGAGGCAGTT	CTGTTTACCA	GGAAGCCATG	AATCAACCAG	GCCACCTTAG	ACTCTTTGTG	5220

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SEQUENCE VERIFICATION REPORT
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Original Text